

## SEQUENCE LISTING

<110> Institut National de la Santé et de la Recherche Médicale -  
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<120> Method for demonstration of a molecular event in a cell by means of  
 fluorescent marker proteins

<130> D20600

<140> PCT/FR2004/001678  
 <141> 2004 - 06 - 30

<150> FR 03/08 186  
 <151> 2003-07-04

<160> 14

<170> PatentIn version 3.2

<210> 1  
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<220>  
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 gga ggt ggc gga tcc ttc gag ccg tcc gaa act ctg atc act acc gtt 96  
 Gly Gly Gly Gly Ser Phe Glu Pro Ser Glu Thr Leu Ile Thr Thr Val  
 20 25 30  
 gaa tcg aac tcg agt tgg tgg act aac tgg gtt atc cct gcg atc tct 144  
 Glu Ser Asn Ser Ser Trp Trp Thr Asn Trp Val Ile Pro Ala Ile Ser  
 35 40 45  
 gct ctg gtt gta gcg ctg atg tac ccg cgt taatgactgc agtctagagg g 195  
 Ala Leu Val Val Ala Leu Met Tyr Arg Arg  
 50 55

<210> 2  
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213> Artificial sequence

<220>

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Glu	Ser	Asn	Ser	Ser	Trp	Trp	Thr	Asn	Trp	Val	Ile	Pro	Ala	Ile	Ser	
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<210> 3

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<223> Caspase 3 probe DEVD-SNAP-25(80-136)

<220>

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<222> (1) .. (291)

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1				5					10					15		
gga	ggt	ggc	gga	tcc	ttc	gag	ccg	tcc	gaa	act	ctg	atc	act	acc	gtt	96
Gly	Gly	Gly	Gly	Ser	Phe	Glu	Pro	Ser	Glu	Thr	Leu	Ile	Thr	Thr	Val	
			20					25					30			
gaa	tcg	aac	tcg	agt	atg	gac	cta	gga	aaa	ttc	tgc	ggg	ctt	tgt	gtg	144
Glu	Ser	Asn	Ser	Ser	Met	Asp	Leu	Gly	Lys	Phe	Cys	Gly	Leu	Cys	Val	
		35					40					45				
tgt	ccc	tgt	aac	aag	ctt	aaa	tcc	agt	gat	gct	tac	aaa	aaa	gcc	tgg	192
Cys	Pro	Cys	Asn	Lys	Leu	Lys	Ser	Ser	Asp	Ala	Tyr	Lys	Lys	Ala	Trp	
	50					55				60						
ggc	aat	aat	cag	gat	gga	gta	gtg	gcc	agc	cag	cct	gcc	cgt	gtg	gtg	240
Gly	Asn	Asn	Gln	Asp	Gly	Val	Val	Ala	Ser	Gln	Pro	Ala	Arg	Val	Val	
65					70				75					80		
gat	gaa	cgg	gag	cag	atg	gcc	atc	agt	ggt	ggc	ttc	atc	cgc	aga	cgc	288
Asp	Glu	Arg	Glu	Gln	Met	Ala	Ile	Ser	Gly	Gly	Phe	Ile	Arg	Arg	Arg	
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gtc	taa															294
Val																

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Gly	Gly	Gly	Gly	Ser	Phe	Glu	Pro	Ser	Glu	Thr	Leu	Ile	Thr	Thr	Val	
			20					25					30			
Glu	Ser	Asn	Ser	Ser	Met	Asp	Leu	Gly	Lys	Phe	Cys	Gly	Leu	Cys	Val	
		35					40				45					
Cys	Pro	Cys	Asn	Lys	Leu	Lys	Ser	Ser	Asp	Ala	Tyr	Lys	Lys	Ala	Trp	
	50					55				60						
Gly	Asn	Asn	Gln	Asp	Gly	Val	Val	Ala	Ser	Gln	Pro	Ala	Arg	Val	Val	
65					70					75					80	
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Val

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1				5					10					15		
gga	ggt	ggc	gga	tcc	ttc	gag	ccg	tcc	gaa	act	ctg	atc	act	acc	gtt	96
Gly	Gly	Gly	Gly	Ser	Phe	Glu	Pro	Ser	Glu	Thr	Leu	Ile	Thr	Thr	Val	
			20					25					30			
gaa	tcg	aac	tcg	agt	atg	gac	cta	gga	aaa	ttc	tgc	ggg	ctt	tgt	gtg	144
Glu	Ser	Asn	Ser	Ser	Met	Asp	Leu	Gly	Lys	Phe	Cys	Gly	Leu	Cys	Val	
		35					40				45					
tgt	ccc	tgt	aac	aag	ctt	aaa	tcc	agt	gat	gct	tac	aaa	aaa	gcc	tgg	192
Cys	Pro	Cys	Asn	Lys	Leu	Lys	Ser	Ser	Asp	Ala	Tyr	Lys	Lys	Ala	Trp	
	50					55				60						
ggc	aat	aat	cag	gat	gga	gta	gtg	gcc	agc	cag	cct	gcc	cgt	gtg	gtg	240

Gly Asn Asn Gln Asp Gly Val Val Ala Ser Gln Pro Ala Arg Val Val  
 65 70 75 80

gat gaa cgg gag cag atg gcc atc agt ggt ggc ttc atc cgc aga cgc 288  
 Asp Glu Arg Glu Gln Met Ala Ile Ser Gly Gly Phe Ile Arg Arg Arg  
 85 90 95

gtc taa 294  
 Val

<210> 6  
 <211> 97  
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<220>  
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Gly Gly Gly Gly Ser Phe Glu Pro Ser Glu Thr Leu Ile Thr Thr Val  
 20 25 30

Glu Ser Asn Ser Ser Met Asp Leu Gly Lys Phe Cys Gly Leu Cys Val  
 35 40 45

Cys Pro Cys Asn Lys Leu Lys Ser Ser Asp Ala Tyr Lys Lys Ala Trp  
 50 55 60

Gly Asn Asn Gln Asp Gly Val Val Ala Ser Gln Pro Ala Arg Val Val  
 65 70 75 80

Asp Glu Arg Glu Gln Met Ala Ile Ser Gly Gly Phe Ile Arg Arg Arg  
 85 90 95

Val

<210> 7  
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 Glu Gly Gly Gly Gly Ser Asp Glu Val Asp Ser Gly Gly Gly Gly Ser  
 1 5 10 15

gga ggt ggc gga tcc atg aca gat gcc gct gtg tcc ttc gcc aag gac 96

Gly	Gly	Gly	Gly	Ser	Met	Thr	Asp	Ala	Ala	Val	Ser	Phe	Ala	Lys	Asp	
			20					25					30			
ttc	ttg	gcc	ggg	gga	gtg	gcc	gca	gcc	atc	tcc	aag	aca	gcg	gta	gca	144
Phe	Leu	Ala	Gly	Gly	Val	Ala	Ala	Ala	Ile	Ser	Lys	Thr	Ala	Val	Ala	
		35					40					45				
ccc	atc	gag	agg	gtc	aag	ctg	ctg	ctg	cag	gtg	cag	cat	gcc	agc	aag	192
Pro	Ile	Glu	Arg	Val	Lys	Leu	Leu	Leu	Gln	Val	Gln	His	Ala	Ser	Lys	
	50					55					60					
caa	atc	acg	gca	gat	aag	caa	tac	aag	ggc	atc	ata	gac	tgc	gtg	gtt	240
Gln	Ile	Thr	Ala	Asp	Lys	Gln	Tyr	Lys	Gly	Ile	Ile	Asp	Cys	Val	Val	
65					70					75					80	
cgt	atc	ccc	aag	gaa	cag	gga	gtc	ctg	tcc	ttc	tgg	cgt	ggg	aac	ctg	288
Arg	Ile	Pro	Lys	Glu	Gln	Gly	Val	Leu	Ser	Phe	Trp	Arg	Gly	Asn	Leu	
				85					90					95		
gcc	aat	gtc	atc	aga	tac	ttc	ccc	acc	cag	gct	ctc	aac	ttt	gcc	ttc	336
Ala	Asn	Val	Ile	Arg	Tyr	Phe	Pro	Thr	Gln	Ala	Leu	Asn	Phe	Ala	Phe	
				100				105					110			
aaa	gat	aaa	tac	aag	cag	atc	ttt	ctg	ggg	ggg	gtg	gac	aag	agg	acc	384
Lys	Asp	Lys	Tyr	Lys	Gln	Ile	Phe	Leu	Gly	Gly	Val	Asp	Lys	Arg	Thr	
		115					120					125				
cag	ttc	tgg	cgc	tac	ttt	gca	ggg	aac	ctg	gca	tca	ggg	ggg	gcc	gct	432
Gln	Phe	Trp	Arg	Tyr	Phe	Ala	Gly	Asn	Leu	Ala	Ser	Gly	Gly	Ala	Ala	
	130					135					140					
ggg	gct	aca	tcc	ttg	tgc	ttt	gtg	tac	cct	ctt	gat	ttt	gcc	cgt	acc	480
Gly	Ala	Thr	Ser	Leu	Cys	Phe	Val	Tyr	Pro	Leu	Asp	Phe	Ala	Arg	Thr	
145					150					155					160	
cgt	cta	gca	gct	gat	gtg	ggc	aaa	gct	gga	gct	gaa	agg	gaa	ttc	aaa	528
Arg	Leu	Ala	Ala	Asp	Val	Gly	Lys	Ala	Gly	Ala	Glu	Arg	Glu	Phe	Lys	
				165					170					175		
ggc	ctt	ggg	gac	tgc	ctg	gtt	aag	atc	tac	aaa	tct	gat	ggg	att	aag	576
Gly	Leu	Gly	Asp	Cys	Leu	Val	Lys	Ile	Tyr	Lys	Ser	Asp	Gly	Ile	Lys	
			180					185					190			
ggc	ctg	tac	caa	ggc	ttt	aat	gtg	tca	gta	cag	ggc	att	atc	atc	tac	624
Gly	Leu	Tyr	Gln	Gly	Phe	Asn	Val	Ser	Val	Gln	Gly	Ile	Ile	Ile	Tyr	
		195					200					205				
cga	gct	gcc	tac	ttt	ggg	atc	tat	gac	act	gca	aag	gga	atg	ctc	cca	672
Arg	Ala	Ala	Tyr	Phe	Gly	Ile	Tyr	Asp	Thr	Ala	Lys	Gly	Met	Leu	Pro	
		210				215					220					
gat	ccc	aag	aat	act	cac	atc	ttc	atc	agc	tgg	atg	att	gca	cag	tct	720
Asp	Pro	Lys	Asn	Thr	His	Ile	Phe	Ile	Ser	Trp	Met	Ile	Ala	Gln	Ser	
225					230					235					240	
gtc	act	gct	gtc	gct	ggc	ctg	act	tcc	tat	cct	ttt	gac	acg	gtt	cgc	768
Val	Thr	Ala	Val	Ala	Gly	Leu	Thr	Ser	Tyr	Pro	Phe	Asp	Thr	Val	Arg	
				245					250					255		
cgt	cgt	atg	atg	atg	cag	tct	gga	cgc	aaa	gga	act	gat	atc	atg	tac	816
Arg	Arg	Met	Met	Met	Gln	Ser	Gly	Arg	Lys	Gly	Thr	Asp	Ile	Met	Tyr	

260	265	270	
aca ggc acg ctt gac tgc tgg cgg aag atc gcg cgc gat gaa ggg agc			864
Thr Gly Thr Leu Asp Cys Trp Arg Lys Ile Ala Arg Asp Glu Gly Ser			
275	280	285	
aag gct ttt ttc aag ggc gca tgg tcc aac gtt ctc aga ggc atg ggt			912
Lys Ala Phe Phe Lys Gly Ala Trp Ser Asn Val Leu Arg Gly Met Gly			
290	295	300	
ggc gcc ttt gtg ctt gtc ttg tat gat gag atc aag aaa tac aca taa			960
Gly Ala Phe Val Leu Val Leu Tyr Asp Glu Ile Lys Lys Tyr Thr			
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Phe Leu Ala Gly Gly Val Ala Ala Ala Ile Ser Lys Thr Ala Val Ala			
35	40	45	
Pro Ile Glu Arg Val Lys Leu Leu Leu Gln Val Gln His Ala Ser Lys			
50	55	60	
Gln Ile Thr Ala Asp Lys Gln Tyr Lys Gly Ile Ile Asp Cys Val Val			
65	70	75	80
Arg Ile Pro Lys Glu Gln Gly Val Leu Ser Phe Trp Arg Gly Asn Leu			
85	90	95	
Ala Asn Val Ile Arg Tyr Phe Pro Thr Gln Ala Leu Asn Phe Ala Phe			
100	105	110	
Lys Asp Lys Tyr Lys Gln Ile Phe Leu Gly Gly Val Asp Lys Arg Thr			
115	120	125	
Gln Phe Trp Arg Tyr Phe Ala Gly Asn Leu Ala Ser Gly Gly Ala Ala			
130	135	140	
Gly Ala Thr Ser Leu Cys Phe Val Tyr Pro Leu Asp Phe Ala Arg Thr			
145	150	155	160
Arg Leu Ala Ala Asp Val Gly Lys Ala Gly Ala Glu Arg Glu Phe Lys			
165	170	175	
Gly Leu Gly Asp Cys Leu Val Lys Ile Tyr Lys Ser Asp Gly Ile Lys			
180	185	190	

Gly Leu Tyr Gln Gly Phe Asn Val Ser Val Gln Gly Ile Ile Ile Tyr  
 195 200 205  
 Arg Ala Ala Tyr Phe Gly Ile Tyr Asp Thr Ala Lys Gly Met Leu Pro  
 210 215 220  
 Asp Pro Lys Asn Thr His Ile Phe Ile Ser Trp Met Ile Ala Gln Ser  
 225 230 235 240  
 Val Thr Ala Val Ala Gly Leu Thr Ser Tyr Pro Phe Asp Thr Val Arg  
 245 250 255  
 Arg Arg Met Met Met Gln Ser Gly Arg Lys Gly Thr Asp Ile Met Tyr  
 260 265 270  
 Thr Gly Thr Leu Asp Cys Trp Arg Lys Ile Ala Arg Asp Glu Gly Ser  
 275 280 285  
 Lys Ala Phe Phe Lys Gly Ala Trp Ser Asn Val Leu Arg Gly Met Gly  
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 Gly Ala Phe Val Leu Val Leu Tyr Asp Glu Ile Lys Lys Tyr Thr  
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<210> 9

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<212> DNA

<213> Artificial sequence

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<223> Caspase 3 probe H2B-DEVD

<220>

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<222> (1)..(411)

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 1 5 10 15

aag gcg gtg act aag gcg cag aag aaa ggc ggc aag aag cgc aag cgc 96  
 Lys Ala Val Thr Lys Ala Gln Lys Lys Gly Gly Lys Lys Arg Lys Arg  
 20 25 30

agc cgc aag gag agc tat tcc atc tat gtg tac aag gtt ctg aag cag 144  
 Ser Arg Lys Glu Ser Tyr Ser Ile Tyr Val Tyr Lys Val Leu Lys Gln  
 35 40 45

gtc cac cct gac acc ggc att tcg tcc aag gcc atg ggc atc atg aat 192  
 Val His Pro Asp Thr Gly Ile Ser Ser Lys Ala Met Gly Ile Met Asn  
 50 55 60

tcg ttt gtg aac gac att ttc gag cgc atc gca ggt gag gct tcc cgc 240  
 Ser Phe Val Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala Ser Arg  
 65 70 75 80

ctg gcg cat tac aac aag cgc tcg acc atc acc tcc agg gag atc cag 288  
 Leu Ala His Tyr Asn Lys Arg Ser Thr Ile Thr Ser Arg Glu Ile Gln  
 85 90 95

acg gcc gtg cgc ctg ctg ctg cct ggg gag ttg gcc aag cac gcc gtg 336  
 Thr Ala Val Arg Leu Leu Leu Pro Gly Glu Leu Ala Lys His Ala Val  
                   100                  105                  110

tcc gag ggt act aag gcc atc acc aag tac acc agc gct aag gat cca 384  
 Ser Glu Gly Thr Lys Ala Ile Thr Lys Tyr Thr Ser Ala Lys Asp Pro  
                   115                  120                  125

ccg gtc gat gaa gtc gat gcc acc atg 411  
 Pro Val Asp Glu Val Asp Ala Thr Met  
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<212> PRT

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Lys Ala Val Thr Lys Ala Gln Lys Lys Gly Gly Lys Lys Arg Lys Arg  
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Ser Arg Lys Glu Ser Tyr Ser Ile Tyr Val Tyr Lys Val Leu Lys Gln  
                   35                  40                  45

Val His Pro Asp Thr Gly Ile Ser Ser Lys Ala Met Gly Ile Met Asn  
                   50                  55                  60

Ser Phe Val Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala Ser Arg  
 65                  70                  75                  80

Leu Ala His Tyr Asn Lys Arg Ser Thr Ile Thr Ser Arg Glu Ile Gln  
                   85                  90                  95

Thr Ala Val Arg Leu Leu Leu Pro Gly Glu Leu Ala Lys His Ala Val  
                   100                  105                  110

Ser Glu Gly Thr Lys Ala Ile Thr Lys Tyr Thr Ser Ala Lys Asp Pro  
                   115                  120                  125

Pro Val Asp Glu Val Asp Ala Thr Met  
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<210> 11

<211> 414

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<220>

<223> Caspase 2 probe H2B-VDVAD

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (414)

&lt;400&gt; 11

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1 5 10 15	
aag gcg gtg act aag gcg cag aag aaa ggc ggc aag aag cgc aag cgc	96
Lys Ala Val Thr Lys Ala Gln Lys Lys Gly Gly Lys Lys Arg Lys Arg	
20 25 30	
agc cgc aag gag agc tat tcc atc tat gtg tac aag gtt ctg aag cag	144
Ser Arg Lys Glu Ser Tyr Ser Ile Tyr Val Tyr Lys Val Leu Lys Gln	
35 40 45	
gtc cac cct gac acc ggc att tcg tcc aag gcc atg ggc atc atg aat	192
Val His Pro Asp Thr Gly Ile Ser Ser Lys Ala Met Gly Ile Met Asn	
50 55 60	
tcg ttt gtg aac gac att ttc gag cgc atc gca ggt gag gct tcc cgc	240
Ser Phe Val Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala Ser Arg	
65 70 75 80	
ctg gcg cat tac aac aag cgc tcg acc atc acc tcc agg gag atc cag	288
Leu Ala His Tyr Asn Lys Arg Ser Thr Ile Thr Ser Arg Glu Ile Gln	
85 90 95	
acg gcc gtg cgc ctg ctg ctg cct ggg gag ttg gcc aag cac gcc gtg	336
Thr Ala Val Arg Leu Leu Leu Pro Gly Glu Leu Ala Lys His Ala Val	
100 105 110	
tcc gag ggt act aag gcc atc acc aag tac acc agc gct aag gat cca	384
Ser Glu Gly Thr Lys Ala Ile Thr Lys Tyr Thr Ser Ala Lys Asp Pro	
115 120 125	
ccg gtc gtc gac gtc gcc gat gcc acc atg	414
Pro Val Val Asp Val Ala Asp Ala Thr Met	
130 135	

&lt;210&gt; 12

&lt;211&gt; 138

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Caspase 2 probe H2B-VDVAD

&lt;400&gt; 12

Met Pro Glu Pro Ala Lys Ser Ala Pro Ala Pro Lys Lys Gly Ser Lys	
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Lys Ala Val Thr Lys Ala Gln Lys Lys Gly Gly Lys Lys Arg Lys Arg	
20 25 30	
Ser Arg Lys Glu Ser Tyr Ser Ile Tyr Val Tyr Lys Val Leu Lys Gln	
35 40 45	

Val His Pro Asp Thr Gly Ile Ser Ser Lys Ala Met Gly Ile Met Asn  
 50 55 60

Ser Phe Val Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala Ser Arg  
 65 70 75 80

Leu Ala His Tyr Asn Lys Arg Ser Thr Ile Thr Ser Arg Glu Ile Gln  
 85 90 95

Thr Ala Val Arg Leu Leu Leu Pro Gly Glu Leu Ala Lys His Ala Val  
 100 105 110

Ser Glu Gly Thr Lys Ala Ile Thr Lys Tyr Thr Ser Ala Lys Asp Pro  
 115 120 125

Pro Val Val Asp Val Ala Asp Ala Thr Met  
 130 135

<210> 13  
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<220>  
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<400> 3  
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 1 5 10 15

gga ggt ggc gga tcc ttc gag ccg tcc gaa act ctg atc act acc gtt 96  
 Gly Gly Gly Gly Ser Phe Glu Pro Ser Glu Thr Leu Ile Thr Val  
 20 25 30

gaa tcg aac tcg agt tgg tgg act aac tgg gtt atc cct gcg atc tct 144  
 Glu Ser Asn Ser Ser Trp Trp Thr Asn Trp Val Ile Pro Ala Ile Ser  
 35 40 45

gct ctg gtt gta gcg ctg atg tac cgg cgt taa 177  
 Ala Leu Val Val Ala Leu Met Tyr Arg Arg  
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<210> 14  
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<400> 14

Glu Gly Gly Gly Gly Ser Ile Glu Thr Asp Ser Gly Gly Gly Gly Ser  
 1 5 10 15

Gly Gly Gly Gly Ser Phe Glu Pro Ser Glu Thr Leu Ile Thr Thr Val  
20 25 30

Glu Ser Asn Ser Ser Trp Trp Thr Asn Trp Val Ile Pro Ala Ile Ser  
35 40 45

Ala Leu Val Val Ala Leu Met Tyr Arg Arg  
50 55